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=> s methylation or CpG
L1      175663 METHYLATION OR CPG

=> s unstructured (a) nucleic (a) acid
L2            2 UNSTRUCTURED (A) NUCLEIC (A) ACID

=> s l1 and l2
L3            0 L1 AND L2

=> d l2 ibib abs 1-2

L2   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2004:934222  CAPLUS
DOCUMENT NUMBER:          141:389800
TITLE:                    Use of modified nucleotides to reduce unwanted
                          secondary structure in determination of differential
                          gene expression by hybridization
INVENTOR(S):              Sampson, Jeffrey R.; Myerson, Joel
PATENT ASSIGNEE(S):       USA
SOURCE:                   U.S. Pat. Appl. Publ., 27 pp.
                          CODEN: USXXCO
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.           KIND   DATE        APPLICATION NO.         DATE
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     US 2004219532         A1    20041104    US 2003-426490          20030430
PRIORITY APPLN. INFO.:                       US 2003-426490          20030430
AB   The present invention provides an improved method of detecting
     differential expression of a gene of interest using modified nucleotides
     that reduce the levels of secondary structure in a nucleic acid mol.  In
     certain embodiments of the invention, multiple genes of interest are
     provided on the surface of a solid support, such as in the form of a
     microarray.  The presence of carefully chosen unstructured
     nucleic acid bases (UNAs, such as diaminopurine,
     2-thiothymine, 2-thiocytidine, hypoxanthine, and pyrrolopyrimidine) in the
     samples being assayed and in the probes on the surface of the solid
     support provides an internal referenced measurement that is suitable for
     detecting the differential expression of a gene of interest in the
     samples.  Also provided are arrays of pairs UNA probes that are capable of
     detecting differential expression of a particular gene of interest in two
     samples of nucleic acid.

L2   ANSWER 2 OF 2  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2002:553119  CAPLUS
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DOCUMENT NUMBER: 137:106082
TITLE: Enzymatic synthesis of unstructured nucleic acids for improved nanopore sequencing
INVENTOR(S): Sampson, Jeffrey R.
PATENT ASSIGNEE(S): Agilent Technologies, Inc., USA
SOURCE: Eur. Pat. Appl., 33 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
EP 1225234	A2	20020724	EP 2002-250379		20020121
EP 1225234	A3	20040707			
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR					
US 2002197618	A1	20021226	US 2002-52926		20020116
PRIORITY APPLN. INFO.:			US 2001-262973P	P	20010120
			US 2002-52926	A	20020116

AB In one aspect, the present invention provides an improved method of determining the sequence of a nucleic acid polymer using nanopore sequencing. Nanopore sequencing is based on the property of phys. sensing the individual nucleotides (or phys. changes in the environment of the nucleotides i.e. elec. current, phys. force) within an individual single-stranded piece of DNA as it traverses through a nanopore. The present invention generates nucleic acid polymers for nanopore sequencing having multiple tandem repeats of a sequence. A mol. having such tandem repeats reduces the influence of process initiation on the rate of nanopore sequencing. In another aspect, the present invention provides an improved method of sequencing that increases the rate of nanopore sequencing by reducing secondary structure in nucleic acid mols. to be sequenced. Nucleic acid mols. with reduced secondary structure ("unstructured nucleic acids"; UNA) are generated by enzymically incorporating modified nucleotide triphosphates that have a reduced ability to form base pairs with complementary modified and unmodified nucleotides. In a particularly preferred embodiment, unstructured nucleic acids are enzymically synthesized by incorporating triphosphate forms of 2-aminoadenosine, 2-thiothymidine, inosine, pyrrolopyrimidine and combinations therein.